

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/528,708  
Source: PT  
Date Processed by STIC: 3/30/05

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

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## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/528,708</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input checked="" type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line <b>not exceed</b> 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input checked="" type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



PCT

**RAW SEQUENCE LISTING**  
PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005  
TIME: 14:13:00

Input Set : A:\PTO.SR.txt  
Output Set: N:\CRF4\03302005\J528708.raw

3 <110> APPLICANT: Stiftung Alfred-Wegener-Institut fuer Polar- und  
4 Meeresforschung,  
5 Bremerhaven, Germany  
7 <120> TITLE OF INVENTION: A novel nucleic acid sequence coding for a calpain  
8 protease from the coldness-adapted marine fragilaripsis  
9 cylindrus diatom  
11 <130> FILE REFERENCE: AWI 01/0902 DE  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/528,708  
C--> 13 <141> CURRENT FILING DATE: 2005-03-22  
13 <160> NUMBER OF SEQ ID NOS: 4

pp 1/6  
See item 4  
on Error Summary  
sheet

#### ERRORED SEQUENCES

15 <210> SEQ ID NO: 1  
16 <211> LENGTH: 544  
17 <212> TYPE: DNA  
18 <213> ORGANISM: Fragilaripsis cylindrus  
20 <400> SEQUENCE: 1  
E--> 22 gg gaa ttc ggc ctt acg gcc ggg gat gat gga atg ttc tgg att  
23 agt 47 →  
24 Glu Phe Gly Leu Thr Ala Gly Asp Asp Gly Met Phe Trp Ile  
W--> 25 Ser →  
W--> 26 1 5 10  
E--> 27 15  
E--> 29 tgg gag gat gtc ttg ctt tat ttc cgc aat tta caa tta tca tgg  
30 aat 95 →  
31 Trp Glu Asp Val Leu Leu Tyr Phe Arg Asn Leu Gln Leu Ser Trp  
W--> 32 Asn  
W--> 33 20 25 30  
E--> 35 ccc aaa cta ttt gcg tat cgg atg act act cat ggc tta tgg cca  
36 aag 143 →  
37 Pro Lys Leu Phe Ala Tyr Arg Met Thr Thr His Gly Leu Trp Pro  
W--> 38 Lys  
W--> 39 35 40 45  
E--> 41 gat cag gga cca caa aat gat gca ttt aat gtc gga gag aat cca  
42 caa 191 →  
43 Asp Gln Gly Pro Gln Asn Asp Ala Phe Asn Val Gly Glu Asn Pro  
W--> 44 Gln  
W--> 45 50 55 60  
E--> 47 tat atc atg tct ttc tcc gaa aaa gct gta tcg agt aaa cca acg  
48 att 239 →  
49 Tyr Ile Met Ser Phe Ser Glu Lys Ala Val Ser Ser Lys Pro Thr

Does Not Comply  
Corrected Diskette Needed  
See item 1  
on Error  
Summary  
sheet

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005  
TIME: 14:13:00

Input Set : A:\PTO.SR.txt  
Output Set: N:\CRF4\03302005\J528708.raw

W--> 50 Ile  
 W--> 51 65 70 75  
 E--> 53 tgg gta ctg ata tca agg cat gta agc aaa cag gag caa gaa ggt  
     54 gct 287  
     55 Trp Val Leu Ile Ser Arg His Val Ser Lys Gln Glu Gln Glu Gly  
 W--> 56 Ala  
 W--> 57 80 85 90  
 E--> 58 95  
 E--> 60 gag gtg aat gat ttc tta acc ata cat ctc gtt aga aac tcg gct  
     61 aca 335  
     62 Glu Val Asn Asp Phe Leu Thr Ile His Leu Val Arg Asn Ser Ala  
 W--> 63 Thr  
 W--> 64 100 105 110  
 E--> 66 tta gaa aga gtt tgg tat ccc cat gga aaa gca acg att gct aat  
     67 gga 383  
     68 Leu Glu Arg Val Trp Tyr Pro His Gly Lys Ala Thr Ile Ala Asn  
 W--> 69 Gly  
 W--> 72 115 120 125  
 E--> 74 tgc tat aca aac aat cca cac gtg ctt tta cga tac gat gtt tcc  
     75 gga 431  
     76 Cys Tyr Thr Asn Asn Pro His Val Leu Leu Arg Tyr Asp Val Ser  
 W--> 77 Gly  
 W--> 78 130 135 140  
 E--> 80 cct gaa gatcaa ttt atc tcg tta gta ctg tct caa cac gaa aaa  
     81 act 479  
     82 Pro Glu Asp Gln Phe Ile Ser Leu Val Leu Ser Gln His Glu Lys  
 W--> 83 Thr  
 W--> 84 145 150 155  
 E--> 86 caa gat cta tca tac act ctc tct tgt tac tgt acc gaa ccc ttt  
     87 aca 527  
     88 Gln Asp Leu Ser Tyr Thr Leu Ser Cys Tyr Cys Thr Glu Pro Phe  
 W--> 89 Thr  
 W--> 90 160 165 170  
 E--> 91 175  
 E--> 93 cta gga aga cca cca aa  
     94 544  
     95 Leu Gly Arg Pro Pro  
 W--> 96 180  
     99 <210> SEQ ID NO: 2  
     100 <211> LENGTH: 180  
     101 <212> TYPE: DNA  
     102 <213> ORGANISM: Fragilariopsis cylindrus  
     104 <400> SEQUENCE: 2  
     105 Glu Phe Gly Leu Thr Ala Gly Asp Asp Gly Met Phe Trp Ile  
 W--> 106 Ser  
 W--> 107 1 5 10  
 E--> 108 15  
     110 Trp Glu Asp Val Leu Leu Tyr Phe Arg Asn Leu Gln Leu Ser Trp  
 W--> 111 Asn

*All item 1  
on Error sheet  
summary sheet*

*All item 1*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005  
TIME: 14:13:00

Input Set : A:\PTO.SR.txt  
Output Set: N:\CRF4\03302005\J528708.raw

W--> 112                    20                    25                    30  
 114 Pro Lys Leu Phe Ala Tyr Arg Met Thr Thr His Gly Leu Trp Pro  
 W--> 115 Lys  
 W--> 116                    35                    40                    45  
 118 Asp Gln Gly Pro Gln Asn Asp Ala Phe Asn Val Gly Glu Asn Pro  
 W--> 119 Gln  
 W--> 120                    50                    55                    60  
 122 Tyr Ile Met Ser Phe Ser Glu Lys Ala Val Ser Ser Lys Pro Thr  
 W--> 123 Ile  
 W--> 124                    65                    70                    75  
 126 Trp Val Leu Ile Ser Arg His Val Ser Lys Gln Glu Gln Glu Gly  
 W--> 127 Ala  
 W--> 128 80                    85                    90  
 E--> 129 95  
 131 Glu Val Asn Asp Phe Leu Thr Ile His Leu Val Arg Asn Ser Ala  
 W--> 132 Thr  
 W--> 133                    100                    105                    110  
 135 Leu Glu Arg Val Trp Tyr Pro His Gly Lys Ala Thr Ile Ala Asn  
 W--> 136 Gly  
 W--> 137                    115                    120                    125  
 141 Cys Tyr Thr Asn Asn Pro His Val Leu Leu Arg Tyr Asp Val Ser  
 W--> 142 Gly  
 W--> 143                    130                    135                    140  
 145 Pro Glu Asp Gln Phe Ile Ser Leu Val Leu Ser Gln His Glu Lys  
 W--> 146 Thr  
 W--> 147                    145                    150                    155  
 149 Gln Asp Leu Ser Tyr Thr Leu Ser Cys Tyr Cys Thr Glu Pro Phe  
 W--> 150 Thr  
 W--> 151 160                    165                    170  
 E--> 152 175  
 154 Leu Gly Arg Pro Pro  
 E--> 155                    180  
 159 <210> SEQ ID NO: 3  
 160 <211> LENGTH: 544  
 161 <212> TYPE: DNA  
 162 <213> ORGANISM: Fragilariopsis cylindrus  
 164 <400> SEQUENCE: 3  
 E--> 166 tca aac gat ggt gcg caa tac gta gta gag aaa tcg ata ctg gta  
 167 ggt        48  
 168 Ser Asn Asp Gly Ala Gln Tyr Val Val Glu Lys Ser Ile Leu Val  
 W--> 169 Gly  
 W--> 170 1                    5                    10                    15  
 E--> 172 tca gtg aat tat cct gta aaa gat cca ttt aat cag atg aaa cgt  
 173 gga        96  
 174 Ser Val Asn Tyr Pro Val Lys Asp Pro Phe Asn Gln Met Lys Arg  
 W--> 175 Gly  
 W--> 176                    20                    25                    30  
 E--> 178 tca ctt caa acc tac tca gat tca tgg acc gaa cgg gat cgt acc  
 179 tca        144

*See item 1*

*See item 1*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005  
TIME: 14:13:00

Input Set : A:\PTO.SR.txt  
Output Set: N:\CRF4\03302005\J528708.raw

180 Ser Leu Gln Thr Tyr Ser Asp Ser Trp Thr Glu Arg Asp Arg Thr  
W--> 181 Ser  
W--> 182 35 40 45  
E--> 184 ttt gtc atg gca tca cgt aac tta gcc gat ttt cgt aat aac gtg  
185 aag 192  
186 Phe Val Met Ala Ser Arg Asn Leu Ala Asp Phe Arg Asn Asn Val  
W--> 187 Lys  
W--> 188 50 55 60  
E--> 190 gta acg atc gat gct gtt ttt aat cca ctt ttt atc aac gag gaa  
191 tac 240  
192 Val Thr Ile Asp Ala Val Phe Asn Pro Leu Phe Ile Asn Glu Glu  
W--> 193 Tyr  
W--> 194 65 70 75  
E--> 195 80  
E--> 197 aaa tgg atc ttt cgtcaa gaa ggc tgg agg tta gag aca cct gac  
198 aat 288  
199 Lys Trp Ile Phe Arg Gln Glu Gly Trp Arg Leu Glu Thr Pro Asp  
W--> 200 Asn  
W--> 201 85 90 95  
E--> 203 gtc aac cta ctt atc aat ggg aac gct tat gta aac gct aag gcc  
204 gac 336  
205 Val Asn Leu Leu Ile Asn Gly Asn Ala Tyr Val Asn Ala Lys Ala  
W--> 206 Asp  
W--> 207 100 105 110  
E--> 211 cag atg gac ccc caa gag gtt atg ata aag caa atc tac agc aat  
212 ctc 384  
213 Gln Met Asp Pro Gln Glu Val Met Ile Lys Gln Ile Tyr Ser Asn  
W--> 214 Leu  
W--> 215 115 120 125  
E--> 217 ttt gct gat cac gtg tat agc aaa agt cca aaa gga gac gcc gcc  
218 caa 432  
219 Phe Ala Asp His Val Tyr Ser Lys Ser Pro Lys Gly Asp Ala Ala  
W--> 220 Gln  
W--> 221 130 135 140  
E--> 223 gta gtc acc atg aca ttg gca cca agg gcg aat tct gca gat atc  
224 cat 480  
225 Val Val Thr Met Thr Leu Ala Pro Arg Ala Asn Ser Ala Asp Ile  
W--> 226 His  
W--> 227 145 150 155  
E--> 228 160  
E--> 230 cac act ggc ggc cgt ctc gag cat gca tct aga ggg ccc aat tcg  
231 ccc 528  
232 His Thr Gly Gly Arg Leu Glu His Ala Ser Arg Gly Pro Asn Ser  
W--> 233 Pro  
W--> 234 165 170 175  
E--> 236 tat agt gag tcg tat t  
237 544  
238 Tyr Ser Glu Ser Tyr  
W--> 239 180 ~~181~~ ← delete (insert amino acid number under every 5 amino acids) =

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005  
TIME: 14:13:00

Input Set : A:\PTO.SR.txt  
Output Set: N:\CRF4\03302005\J528708.raw

242 <210> SEQ ID NO: 4  
 243 <211> LENGTH: 181  
 244 <212> TYPE: DNA  
 245 <213> ORGANISM: Fragilariopsis cylindrus  
 247 <400> SEQUENCE: 4  
 249 Ser Asn Asp Gly Ala Gln Tyr Val Val Glu Lys Ser Ile Leu Val  
 W--> 250 Gly  
 W--> 251 1 5 10 15  
 253 Ser Val Asn Tyr Pro Val Lys Asp Pro Phe Asn Gln Met Lys Arg  
 W--> 254 Gly  
 W--> 255 20 25 30  
 257 Ser Leu Gln Thr Tyr Ser Asp Ser Trp Thr Glu Arg Asp Arg Thr  
 W--> 258 Ser  
 W--> 259 35 40 45  
 261 Phe Val Met Ala Ser Arg Asn Leu Ala Asp Phe Arg Asn Asn Val  
 W--> 262 Lys  
 W--> 263 50 55 60  
 265 Val Thr Ile Asp Ala Val Phe Asn Pro Leu Phe Ile Asn Glu Glu  
 W--> 266 Tyr  
 W--> 267 65 70 75  
 E--> 268 80  
 270 Lys Trp Ile Phe Arg Gln Glu Gly Trp Arg Leu Glu Thr Pro Asp  
 W--> 271 Asn  
 W--> 272 85 90 95  
 274 Val Asn Leu Leu Ile Asn Gly Asn Ala Tyr Val Asn Ala Lys Ala  
 W--> 275 Asp  
 W--> 276 100 105 110  
 280 Gln Met Asp Pro Gln Glu Val Met Ile Lys Gln Ile Tyr Ser Asn  
 W--> 281 Leu  
 W--> 282 115 120 125  
 284 Phe Ala Asp His Val Tyr Ser Lys Ser Pro Lys Gly Asp Ala Ala  
 W--> 285 Gln  
 W--> 286 130 135 140  
 288 Val Val Thr Met Thr Leu Ala Pro Arg Ala Asn Ser Ala Asp Ile  
 W--> 289 His  
 W--> 290 145 150 155  
 E--> 291 160  
 293 His Thr Gly Gly Arg Leu Glu His Ala Ser Arg Gly Pro Asn Ser  
 W--> 294 Pro  
 W--> 295 165 170 175  
 297 Tyr Ser Glu Ser Tyr *delete "181"*  
 W--> 298 180 ~~181~~ *delete*  
 E--> 301 Attorney Docket 050677-US *delete*

*see p. 1 for more info*

*see p. 6 for more info*

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10/528,708 6

Sequence <sup>Protocol</sup> Listing

<110> Stiftung Alfred-Wegener-Institut fuer Polar- und  
Meeresforschung,  
Bremerhaven, Germany

<120> A novel nucleic acid sequence coding for a calpain  
protease from the coldness-adapted marine *fragilaropsis*  
*cylindrus* diatom

do not  
use  
tables

use a  
fixed-width font  
only

(per 1.823 of Sequence Rules)

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005  
TIME: 14:13:01

Input Set : A:\PTO.SR.txt  
Output Set: N:\CRF4\03302005\J528708.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:22 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:44 SEQ:1  
L:25 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:26 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
M:254 Repeated in SeqNo=1  
L:32 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:33 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:57 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:63 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:69 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:77 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:90 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:108 M:254 E: No. of Bases conflict, this line has no nucleotides.  
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:112 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:120 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
M:254 Repeated in SeqNo=2  
L:132 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:137 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005

TIME: 14:13:01

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03302005\J528708.raw

L:147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:155 M:301 E: (44) No Sequence Data was Shown, SEQ ID:2  
L:155 M:252 E: No. of Seq. differs, <211> LENGTH:Input:180 Found:0 SEQ:2  
L:166 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:45 SEQ:3  
L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
M:254 Repeated in SeqNo=3  
L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:176 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:268 M:254 E: No. of Bases conflict, this line has no nucleotides.  
M:254 Repeated in SeqNo=4  
L:301 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3  
L:301 M:301 E: (44) No Sequence Data was Shown, SEQ ID:4  
L:301 M:252 E: No. of Seq. differs, <211> LENGTH:Input:181 Found:0 SEQ:4